IN THE CLAIMS:

Please insert the following cancellations, amendments and/or additions.

Claims 1-25. (Cancelled).

Claim 26. (Currently Amended) A method of magnifying a signal associated with one or more nucleotide bases of a nucleotide sequence in a target nucleic acid molecule comprising the steps of:

(A) treating said target nucleic acid molecule so that at least a region of said target nucleic acid molecule is converted into a form suitable for binding an adapter molecule (adapter binding region);

wherein said adapter molecule comprises:

(i) one or more ~~of said~~ magnifying tags, or

(ii) a means for attaching one or more of said magnifying tags to said adapter binding region,

wherein said magnifying tag(s) correspond to: (a) one or more nucleotide bases of the adapter binding region or (b) ~~to~~ one or more nucleotide bases ~~in proximity to~~ adjacent to the adapter binding region or (c) one or more nucleotide bases which overlap the adapter binding region;

(B) binding said adapter molecule to at least a portion of said adapter binding region created in step (A) to form a nucleic acid molecule:adapter molecule complex;

(C) optionally, ligating said target nucleic acid molecule to said adapter molecule such that at least said magnifying tag(s) remain associated with said target nucleic acid molecule and to form a ligated nucleic acid molecule:adapter molecule complex;

(D) treating the resulting complex of step (B) or the resulting complex step (C) so that at least another region of said target nucleic acid molecule is converted into a form suitable for binding another adapter molecule, wherein said another region comprises one or more nucleotide bases which are not associated with the magnifying tags of step (B); and thereafter

(E) repeating steps (B) to (D), with the proviso that the adapter molecule in each cycle of steps (B) to (C) binds to a region adjacent to a region of said target nucleic acid molecule to which the adapter molecule of a previous cycle bound, or the adapter molecule in each cycle of steps (B) to (C) binds to a region which overlaps with a region of said target nucleic acid molecule to which the adapter molecule of a previous cycle bound, and wherein the magnifying tags of each cycle of steps (A) to (C) are ligated together,

to thereby magnify said signal.

Claim 27. (Previously Added) The method as claimed in Claim 26, wherein in step (A), said form is a single-stranded nucleic acid molecule.

Claim 28. (Currently Amended) The method as claimed in Claim 26, wherein said magnifying tag(s) correspond to one or more nucleotide bases of said adapter binding region.

Claim 29. (Currently Amended) The method as claimed in Claim 26, wherein each magnifying tag corresponds to at least 2 nucleotide bases in said adapter binding region or to at least 2 nucleotide bases adjacent to said adapter binding region.

Claim 30. (Currently Amended) The method as claimed in Claim 26, wherein said magnifying tags together correspond to at least 2 nucleotide bases in said adapter binding region or to at least 2 nucleotide bases adjacent to said adapter binding region.

Claim 31. (Currently Amended) The method as claimed in Claim 30, wherein said magnifying tags together correspond to at least 4 nucleotide bases in said adapter binding region or to at least 4 nucleotide bases adjacent to said adapter binding region.

Claim 32. (Previously Added) The method as claimed in Claim 26, wherein a chain of magnifying tags are associated with said target nucleic acid molecule.

Claim 33. (Currently Amended) The method as claimed in Claim 32, wherein said chain comprises 4 or more magnifying tags corresponding to at least 4 contiguous nucleotide bases.

Claim 34. (Currently Amended) The method as claimed in Claim 26, wherein said magnifying tags are nucleic acid sequences of at least 2 nucleotide bases in length.

Claim 35. (Currently Amended) The method as claimed in Claim 34, wherein said magnifying tags are nucleic acid sequences of 10 to 30 nucleotide bases in length.

Claim 36. (Previously Added) The method as claimed in Claim 26, wherein said adapter molecule comprises a recognition site for a nuclease, which has a cleavage site separate from its recognition site.

Claim 37. (Previously Added) The method as claimed in Claim 26, wherein said adapter molecule comprises recognition sites for 2 or more nucleases, which have cleavage sites separate from their respective recognition sites, wherein cleavage with said nucleases produces single-stranded regions which are adjacent or overlapping.

Claim 38. (Previously Added) The method as claimed in Claim 26, wherein two or more adapter molecules are bound in step (B).

Claim 39. (Previously Added) The method as claimed in Claim 38, wherein said adapter molecules are bound to overlapping or adjacent regions.

Claim 40. (Currently Amended) The method as claimed in Claim 39, wherein said adapter molecules are bound to overlapping regions thereby allowing the association of more than one magnifying tag with each nucleotide base.

Claim 41. (Previously Added) The method as claimed in Claim 26, wherein step (C) is performed.

Claim 42. (Previously Added) The method as claimed in Claim 26, further comprising the step of:

(F) sequencing the target nucleic acid molecule by identifying the magnifying tags associated with the target nucleic acid molecule.

Claim 43. (Currently Amended) The method as claimed in Claim 42, wherein 2 or more nucleotide bases are sequenced per cycle.

Claim 44. (Currently Amended) The method as claimed in Claim 43, wherein 4 or more nucleotide bases are sequenced per cycle.

Claim 45. (Currently Amended) The method as claimed in Claim 42, wherein the signal associated with each nucleotide base is magnified by increasing the number of times that said nucleotide base appears in said sequence.

Claim 46. (Previously Added) The method as claimed in Claim 42, wherein the resulting magnified signal is converted into readable signals and said sequencing is carried out by assessing the readable signals.

Claim 47. (Previously Added) The method as claimed in Claim 46, wherein each readable signal comprises a pattern made up of a single signal event which creates a unique signal on each magnifying tag.

Claims 48-58. (Cancelled)

Claim 59. (Previously Added) The method as claimed in Claim 26, wherein said method is performed on a sample comprising a heterogeneous mixture of target nucleic acid molecules.

Claim 60. (Previously Added) The method as claimed in Claim 42, wherein said method is performed on a sample comprising a heterogeneous mixture of target nucleic acid molecules.

Claims 61-64. (Cancelled).